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FIG. 1

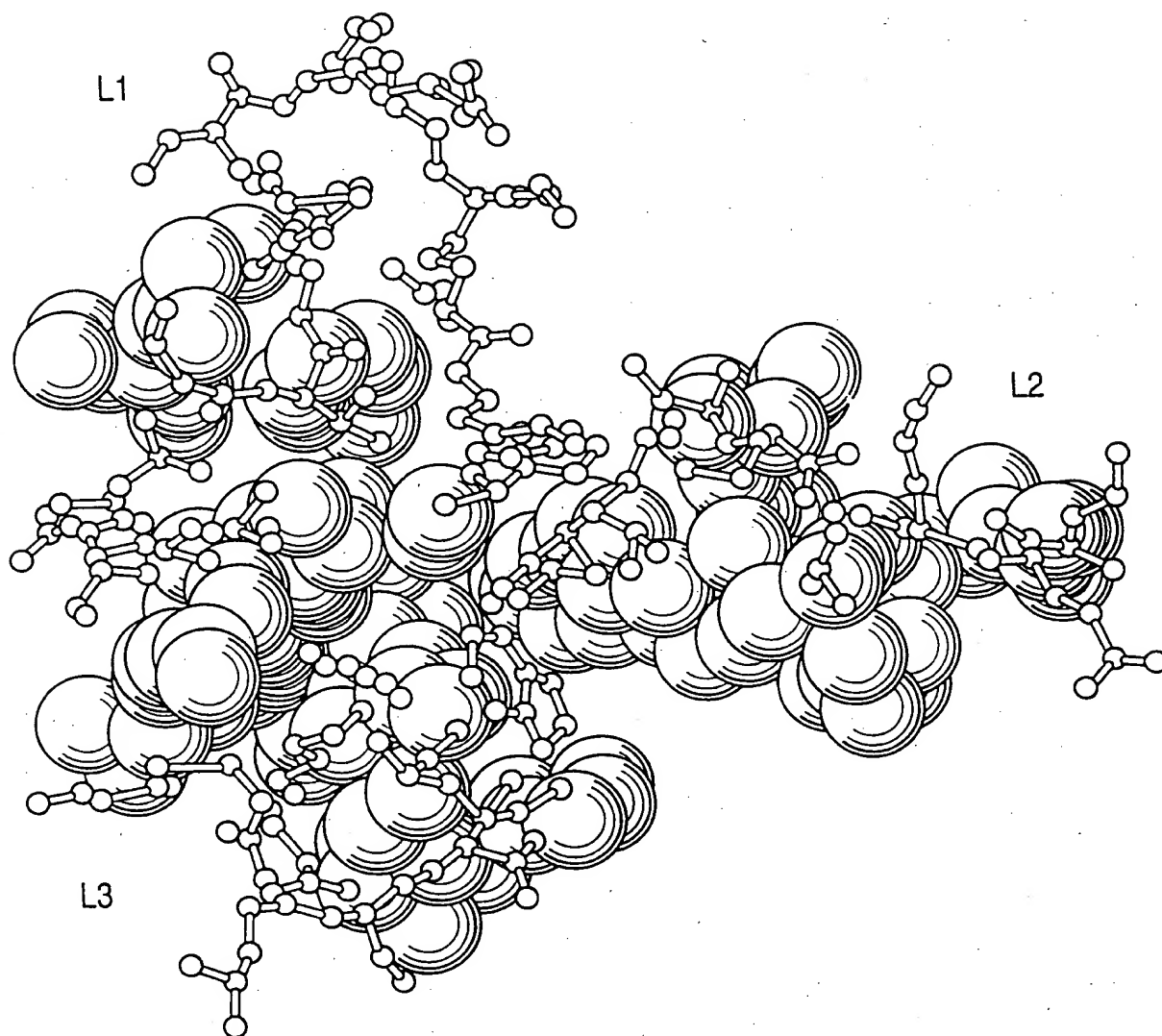
MURINE REIHuVK	FR1 DIQLTQSPSSLA V S A G E N V T M S C -----SA-V-DR-----	L1 KSSQSVLYS A N H K N Y L A -----	FR2 WYQ Q K P G Q S P -----KA-----
MURINE REIHuVK	L2 K L L I Y -----	FR3 G V P D R F T G S G S G T D F T L T I S R V Q V E D L A I Y C -----F---SL-P-I-T-----	L3 H Q Y L S S -----
MURINE REIHuVK	FR4 W T F G G G T K L E I K R -- -- -- -- -- V Q -- --		
MURINE EUHuVH1 EUHuVH2	FR1 Q V Q L Q E S G A E L S K P G A S V K M S C K A S G Y T F T -----Q-----V K -----S-----V-----V Q -----	H1 S Y W L H -----	FR2 W I K Q R P G Q G L E W I G -----VR-A-----VR-A-----
MURINE EUHuVH1 EUHuVH2	H2 Y I N P R N D Y T E Y N Q N F K D -----	FR3 K A T L T A D K S S T A Y M Q L S S L T S E D S A V Y Y C A R -----I---E-TN---E---R---T-F-F-----I---E-TN---E---R---T-F-F-----	
MURINE NEWMHuVH1 NEWMHuVH2	H3 R D I T T F Y -----	FR4 W G Q G T T L T V S S -----V-----V-----	

Title: IMMUNOCONJUGATES AND
HUMANIZED ANTIBODIES SPECIFIC
FOR B-CELL LYMPHOMA AND
LEUKEMIA CELLS

Inventor(s): Shui-on LEUNG et al.

Appl. No.: unassigned

FIG. 2A



Title: IMMUNOCONJUGATES AND
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FIG. 2B

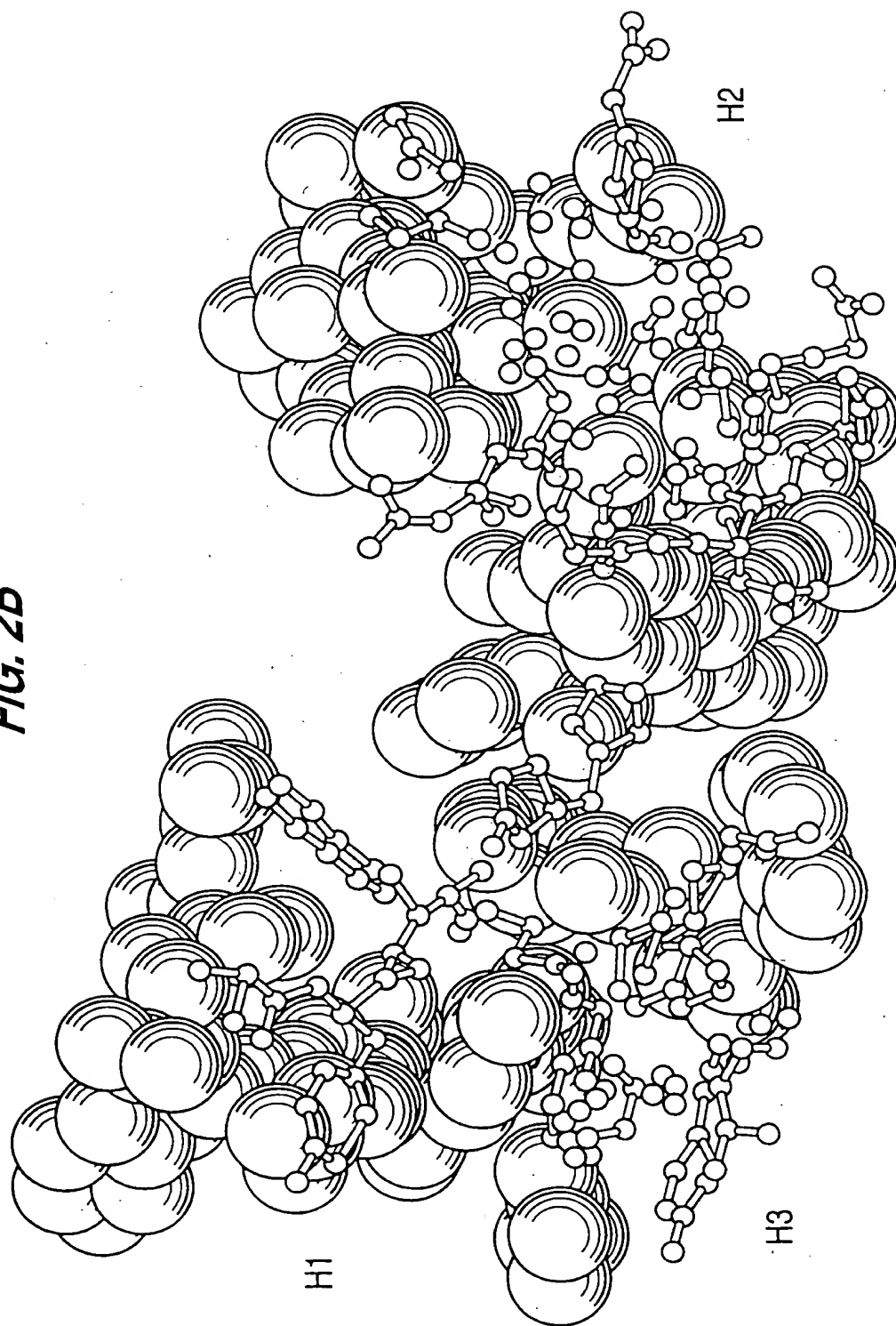


FIG. 3A

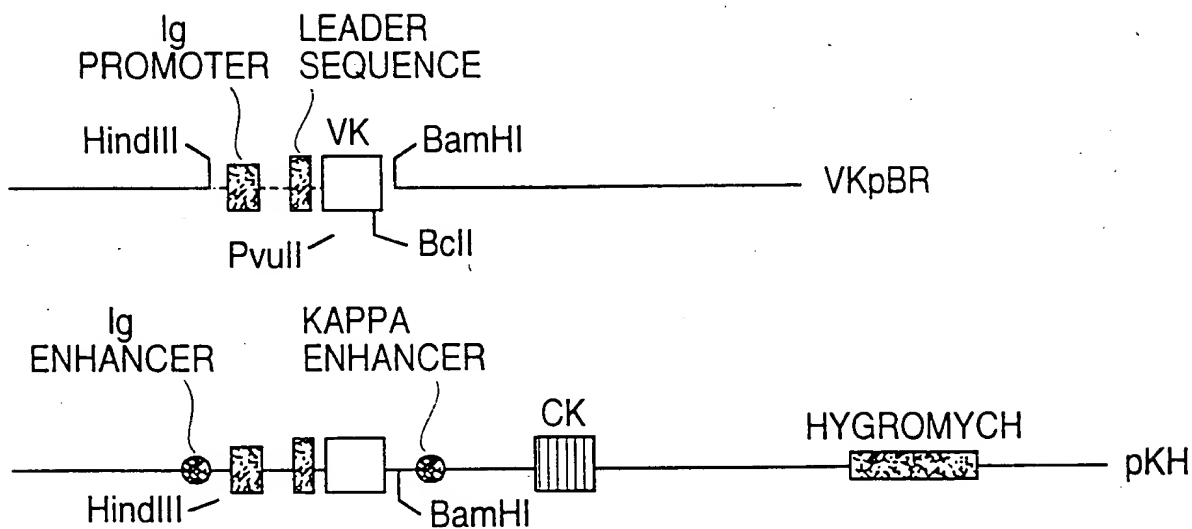


FIG. 3B

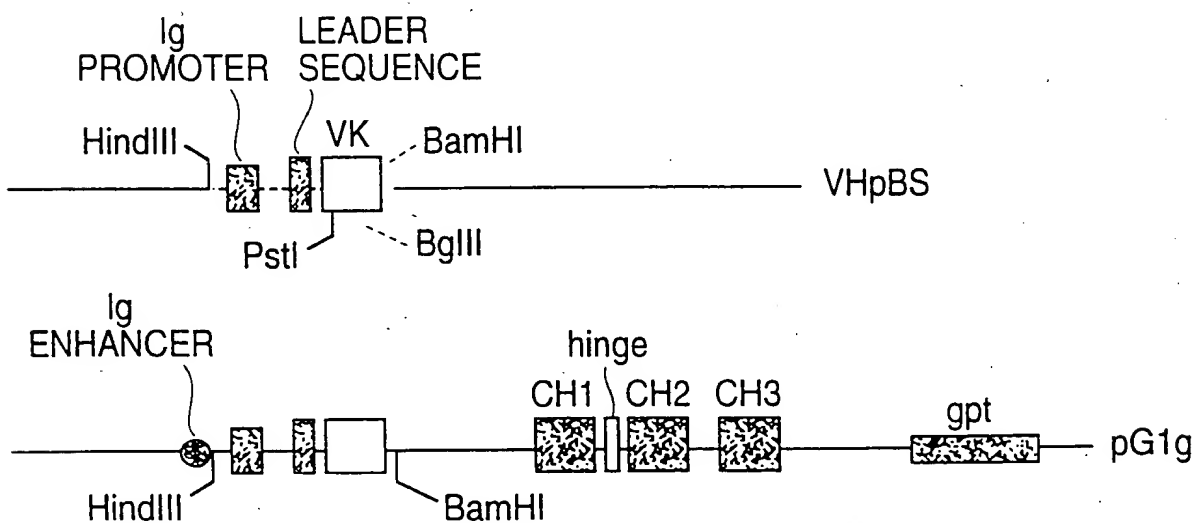


FIG. 4A

GACATTCAGCTGACCCAGTCTCCATCATCTCTGGCTGTGTCTGCAGGAGAAAACGTCACCT
 1-----+-----+-----+-----+-----+-----+-----+-----+ 60
 CTGTAAGTCGACTGGGTCAGAGGTAGTAGAGACCGACACAGACGTCCTCTTTTGCAGTGA
 D I Q L T Q S P S L A V S A G E N V T -
 ATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTGCAAAATCACAAAGAACTACTTGGCC
 61-----+-----+-----+-----+-----+-----+-----+-----+ 120
 TACTCGACATTCAGGTCAGTTTCACAAAATATGTCACGTTTAGTGTTCTTGATGAACCGG
 M S C K S S Q S V L Y S A N H K N Y L A -
 TGGTACCAGCAGAAACACAGGCGAGTCTCCTAACTGCTGATCTACTGGCATCCACTAGG
 121-----+-----+-----+-----+-----+-----+-----+-----+ 180
 ACCATGGTCGCTTTGGTCCCGTCAGAGGATTTGACGACTAGATGACCCGTTAGGTGATCC
 W Y Q Q K P G Q S P K L L I Y W A S T R -
 CDR2
 GAATCTGGTGTCCCTGATCGCTTCACAGGCGGATCTGGACAGATTTTACTCTTACC
 181-----+-----+-----+-----+-----+-----+-----+-----+ 240
 CTTAGACCACAGGACTAGCGAAGTGTCGTCGCCCTAGACCCCTGTCTAAAATGAGAATGG
 E S G V P D R F T G S G S G T D F T L T -
 ATCAGCAGAGTACAAGTTGAAGACCTGGCAATTTATTGTACCAATAACCTCTCCTCG
 241-----+-----+-----+-----+-----+-----+-----+-----+ 300
 TAGTCGTCTCATGTTCAACTTCTGGACCGTTAAATAATAACAGTGGTTATGGAGAGGAGC
 CDR3
 I S R V Q V E D L A I Y Y C H Q Y L S S -
 TGGACGTTCCGGTGGAGGGACCAAGCTGGAGATCAAACGT
 301-----+-----+-----+-----+-----+-----+-----+-----+ 339
 ACCTGCAAGCCACCTCCCTGGTTCGACCTCTAGTTTGCA
 W T F G G G T K L E I K R -

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FIG. 4B

CAGGTCACGCTGCAGGAGTCAGGGCTGAACCTGTCAAAACCTGGGGCCTCAGTGAAGATG
 1
 GTCCAGGTCGACGTCCTCAGTCCCGACTTGACAGTTTGGACCCCGGAGTCACTTCTAC
 Q V Q L Q E S G A E L S K P G A S V K M -
 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGCTGCACCTGGATAAAACAGAGG
 61
 AGGACGTTCCGAAGACCGATGTGGAATGATCGATGACCGACGTGACCTATTTGTCTCTCC
 S C K A S G Y T F T S Y W L H W I K Q R -
 CCTGGACAGGCTCTGGAATGGATTGGATACATTAATCCTAGGAATGATTATACTGAGTAC
 121
 GGACCTGTCCCAGACCTTACCTAACCTATGTAATTAGGATCCTTACTAATATGACTCATG
 P G Q G L E W I G Y I N P R N D Y T E Y -
 AATCAGAACTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC
 181
 TTAGTCTTGAAGTTCCTGTTCCGGTGTAACCTGACGTCGTTTAGGAGGTCGTCTCGGATG
 N Q N F K D K A T L T A D K S S T A Y -
 ATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAAGGAT
 241
 TACGTTGACTCGTTCGGACTGTAGACTCCTGAGACGTCAGATAATGACACGTTCTTCCCTA
 M Q L S S L T S E D S A V Y C A R D -
 ATTACTACGTTCTACTGGGGCCAAGCACCACTCTCACAGTCTCCTCG
 301
 TAATGATGCAAGATGACCCCGGTTCCGTGGTGAGAGTGTACAGAGGAGC

CDR3

I T T F Y
W G Q T L T V S -

FIG. 5A

```

1  GACATCCAGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGTTGAGATAGGGTCACT
   +-----+-----+-----+-----+-----+-----+
60 CTGTAGGTCGACTGGTCAGAGGTAGTAGAGACTCGCGTAGACAACCTCTATCCCAGTGA
   D I Q L T Q S P S S L S A S V G D R V T -
   ATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTGCAAAATCACAAGAACTACTTGGCC
61 +-----+-----+-----+-----+-----+-----+
   TACTCGACATTCAGGTCAGTTTCACAAAATATGTCACGTTTAGTGTTCTTGATGAACCGG
   CDR1
   M S C K S S Q S S V L Y S A N H K N Y L A -
   TGGTACCAGCAGAAACCAGGGAAAGCACCTAAACTGCTGATCTACTGGGCATCCACTAGG
121 +-----+-----+-----+-----+-----+-----+
   ACCATGGTCGCTTTTGGTCCCTTTCTGCGGATTGACGACTAGATGACCCGTAGGTGATCC
   CDR2
   W Y Q Q K P G K A P K L L I Y W A S T R -
   GAATCTGGTGTCCTTCGCGATTCTCTGGCAGCGGATCTGGGACAGATTTTACTTTCACC
181 +-----+-----+-----+-----+-----+-----+
   CTAGACCACAGGGAAGCGCTAAGAGACCGTCGCCCTAGACCCCTGTCTAAAATGAAAGTGG
   E S G V P S R F S G S G S G T D F T F T -
   ATCAGCTCTCTTCAACCAGAAAGACATTGCAACATATATTGTACCAATACCTCTCCTCG
241 +-----+-----+-----+-----+-----+-----+
   TAGTCGAGAGAAGTTGGTCTTCTGTAACGTTGTATAATAACAGTGGTTATGGAGAGGAGC
   CDR3
   I S S L Q P E D I A T Y Y C H Q Y L S S -
   TGGACGTTTCGGTGGAGGGACCAAGGTGCAGATCAAACGT
301 +-----+-----+-----+-----+-----+-----+
   ACCTGCAAGCCACCTCCCTGGTTCACGCTAGTTGCA
   W T F G G G T K V Q I K R

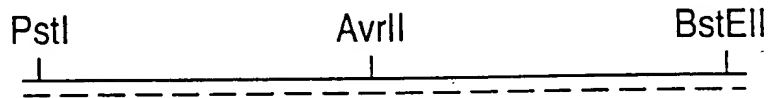
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FIG. 5B

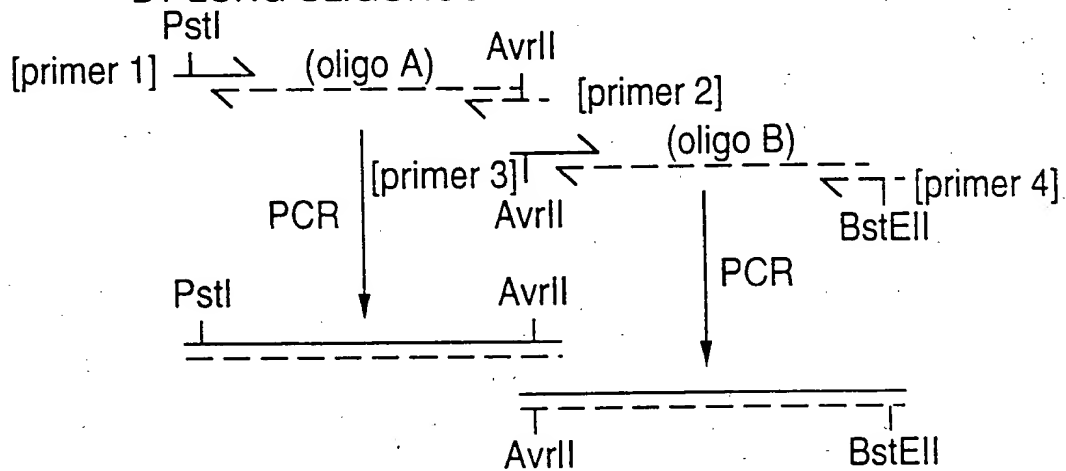
CAGGTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCTGGGTCAATCAGTGAAGGTC
 1-----+-----+-----+-----+-----+-----+ 60
 GTCCAGGTCGACCAGGTTAGTCCCCGACTTCAGTTCTTTGGACCCAGTAGTCACTTCCAG
 Q V Q L V Q S G A E V K K P G S S V K V -
 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGCTGCACTGGGTCAAGCAGGCA
 61-----+-----+-----+-----+-----+-----+ 120
 AGGACGTTCCGAAGACCGATGTGAAATGATCGATGACCGACGTGACCCAGTCCGTCCTCGT
 S C K A S G Y T F T S Y W L H W V R Q A -
 CCTGGACAGGCTCTGGAATGGATTGGATACATAATCCTAGGAATGATTACTGAGTAC
 121-----+-----+-----+-----+-----+-----+ 180
 GGACCTGTCCCAGACCTTACCTAACCTATGTAATTAGGATCCTTACTAATAATGACTCATG
 CDR2
 P G Q G L E W I G Y I N P R N D Y T E Y -
 AATCAGAACTTCAAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTAC
 181-----+-----+-----+-----+-----+-----+ 240
 TTAGTCTTGAAAGTTCTCTGTTCCGGTGTATTGACGTCTGCTAGGTGGTTATGTCGGATG
N Q N F K D K A T I T A D E S T N T A Y -
 ATGGAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTGTGCAAGAAGGAT
 241-----+-----+-----+-----+-----+-----+ 300
 TACCTCGACTCGTCGGACTCCAGACTCCTGTGCCGTAAATAAACAACACGTTCTTCCCTA
 M E L S S L R S E D T A F Y F C A R R D -
 ATTACTAGTTTCTACTGGGCCAAGCACACCGTCAACCGTCTCCCTCG
 301-----+-----+-----+-----+-----+-----+ 348
 TAATGATGCAAGATGACCCCGGTTCCGTGTCAGTGGCAGGAGGAGC
 CDR3
I T T F Y W G Q G T T V T V S S -

FIG. 6

DESIGNED SEQUENCE FOR HUMANIZED LL2 VH DOMAIN:



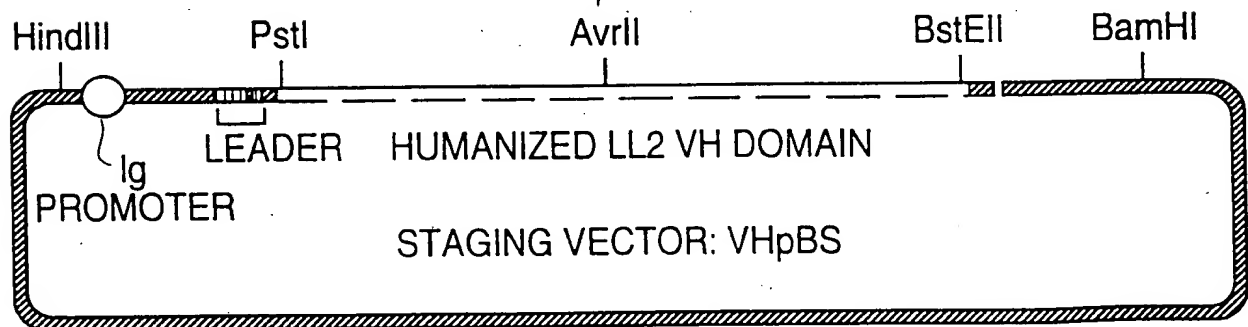
CONSTRUCTION OF THE HUMANIZED LL2 VH DOMAIN
BY LONG OLIGONUCLEOTIDES AND PCR:



PstI/AvrII DIGESTION

BstEII/AvrII DIGESTION

LIGATION TO THE PstI/BstEII
SITES OF THE HEAVY CHAIN
STAGING VECTOR: VHpBS

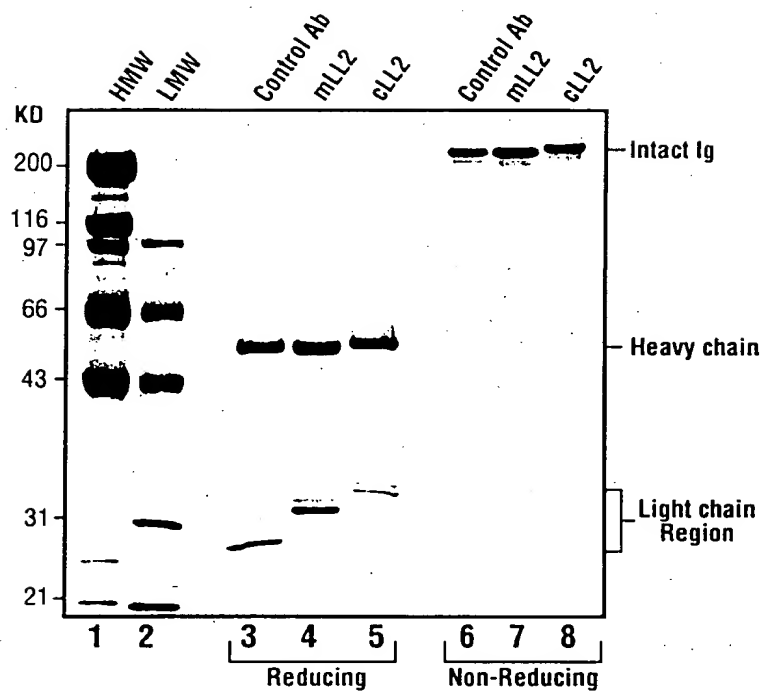


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FIG. 7

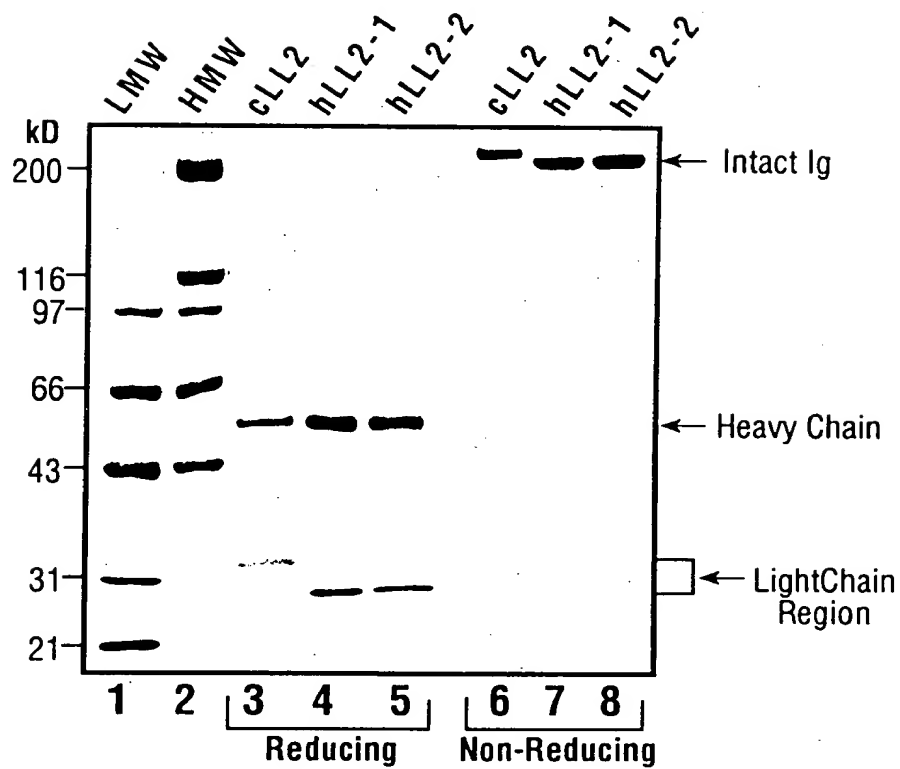


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FIG. 8



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Inventor(s): Shui-on LEUNG et al.

Appl. No.: unassigned

FIG. 9

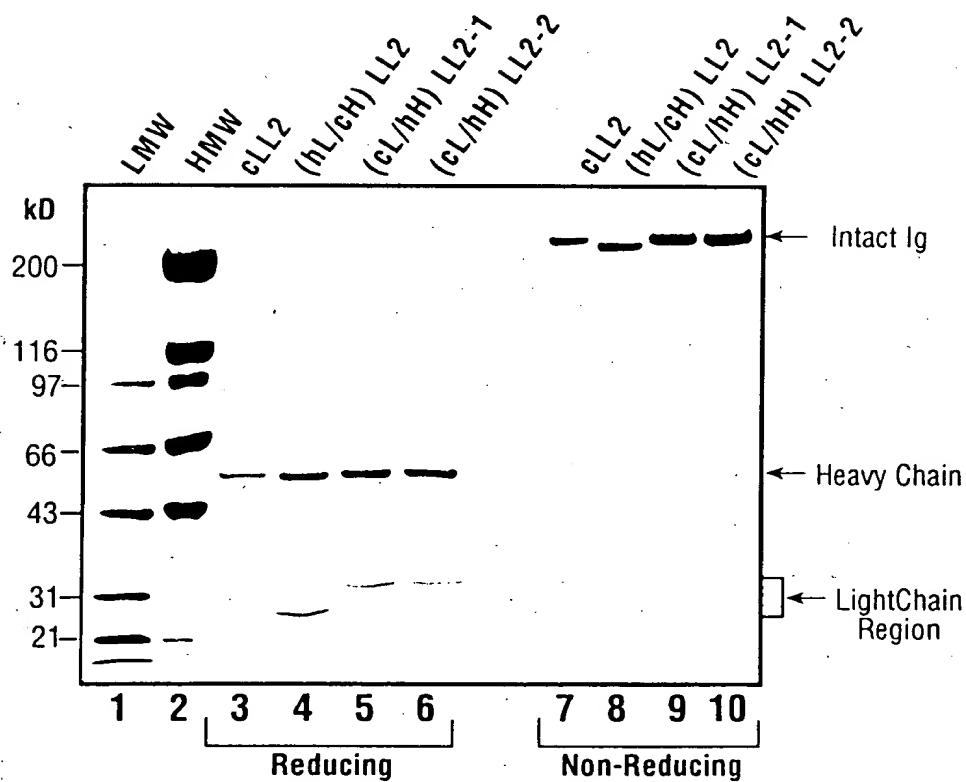


FIG. 10

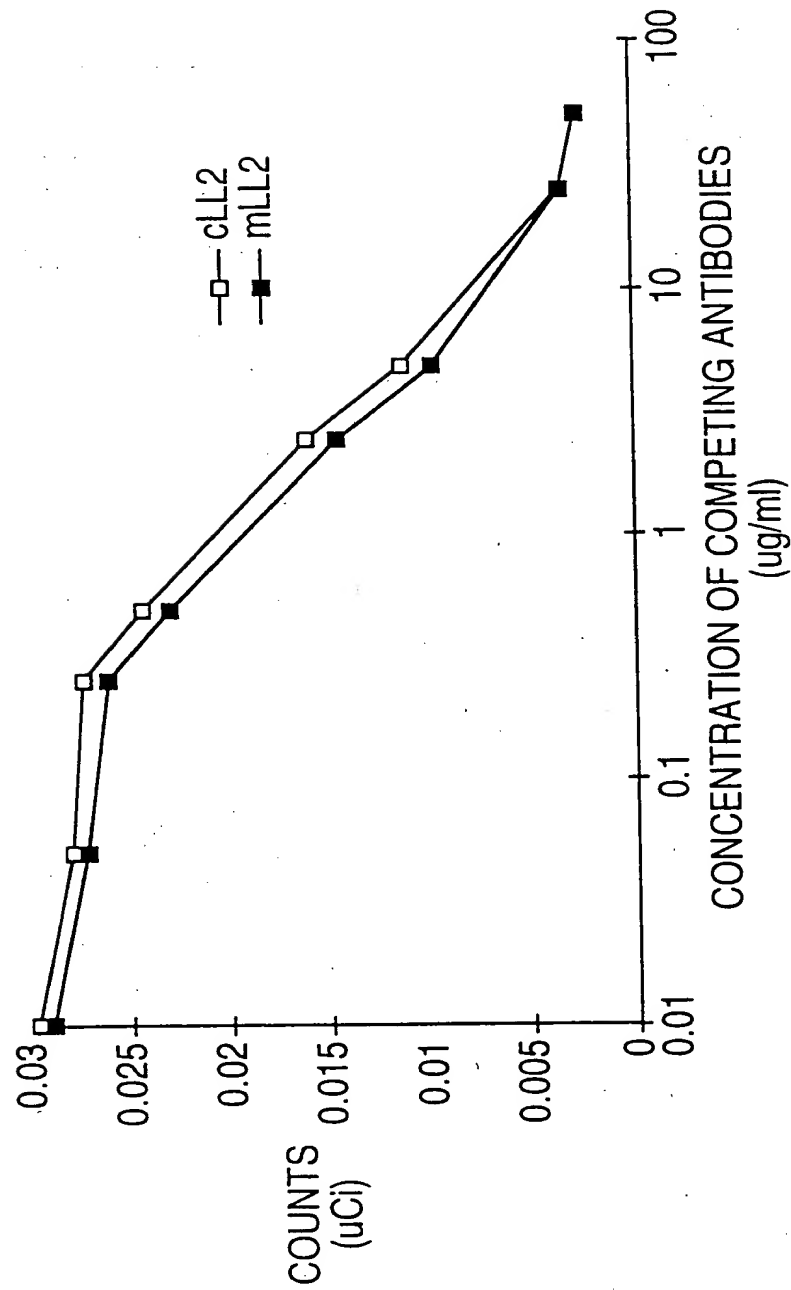


FIG. 11A

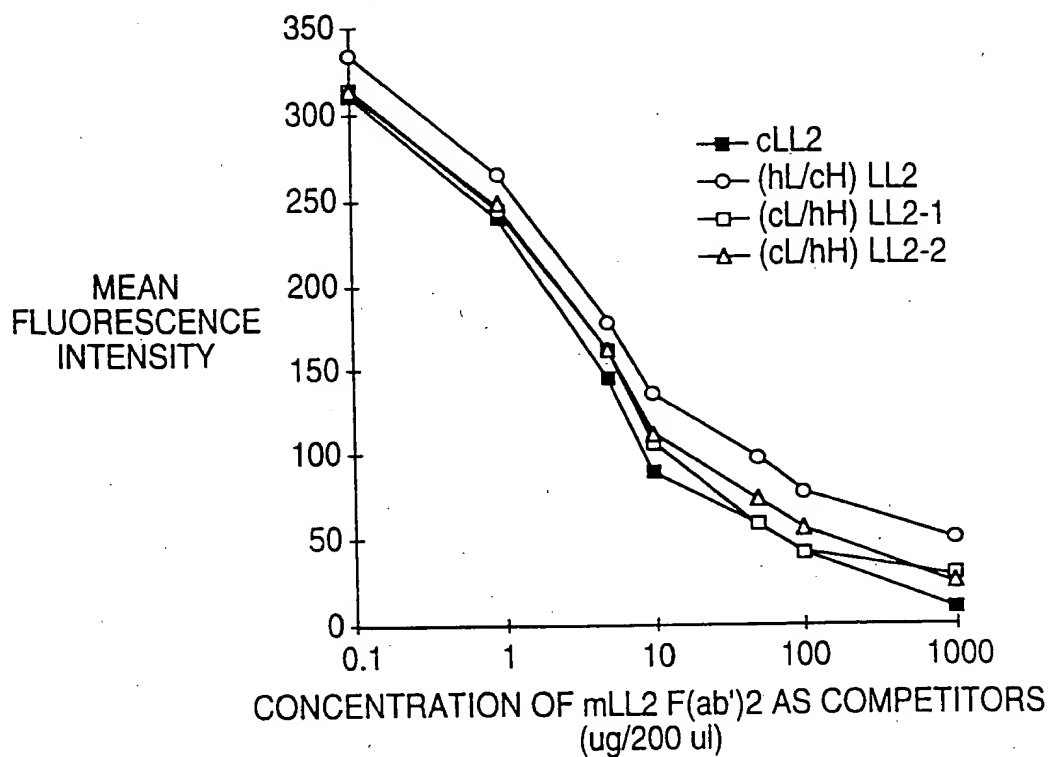
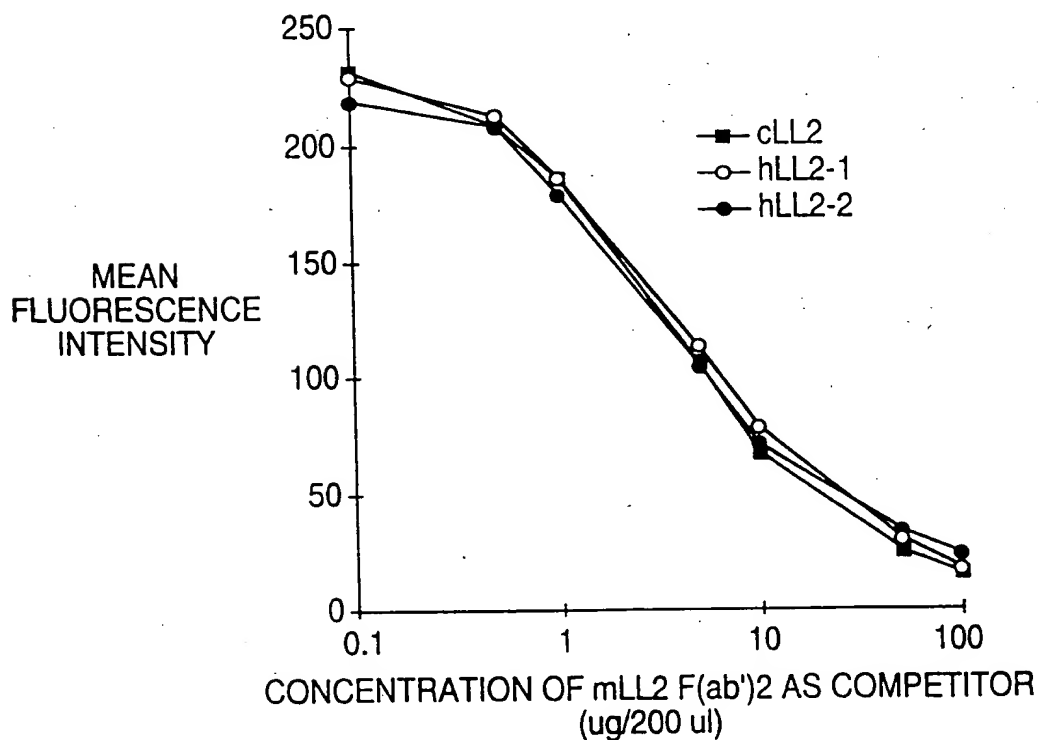


FIG. 11B



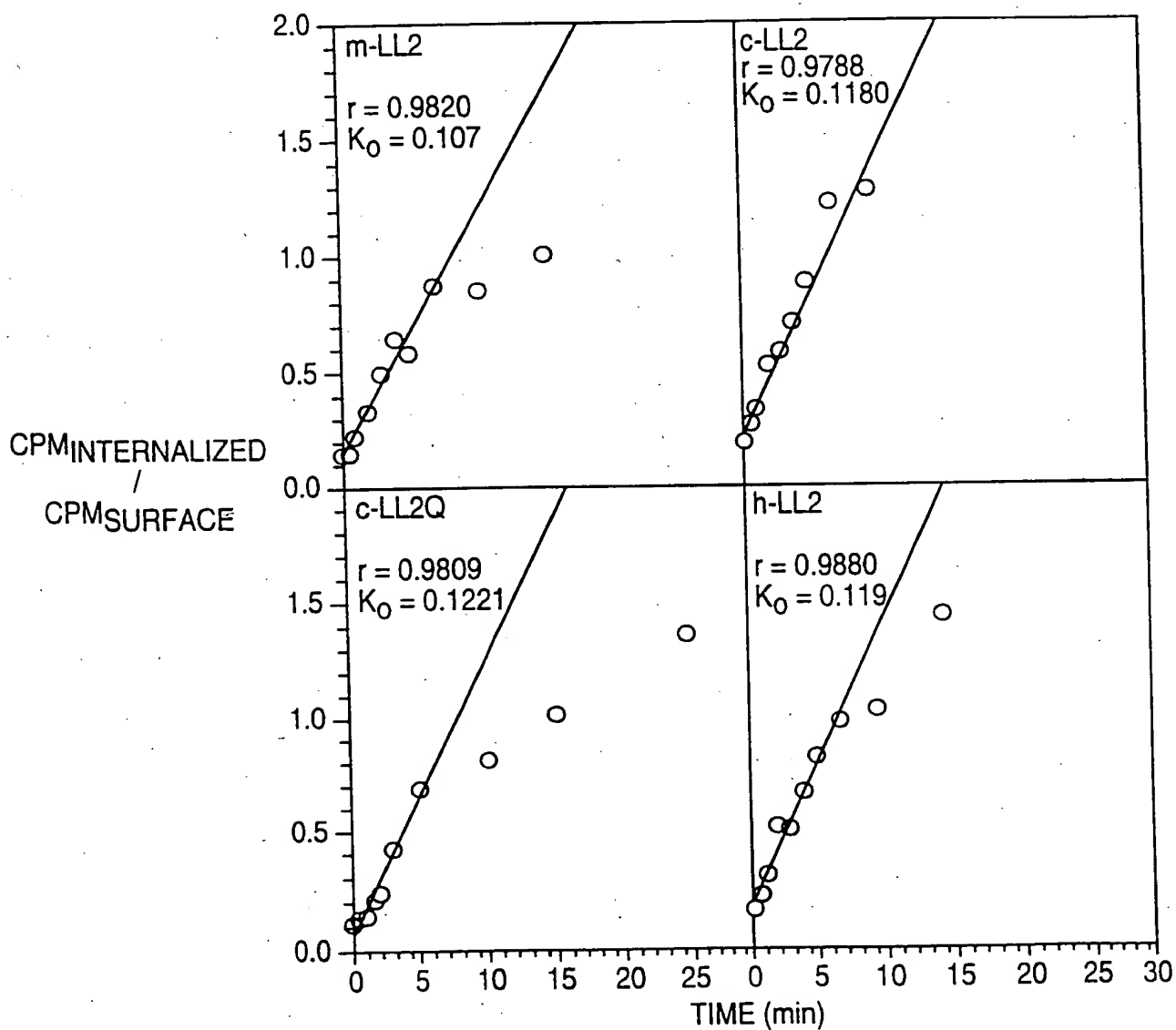
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Appl. No.: unassigned

FIG. 12

INTERNALIZATION: c-LL2, h-LL2 vs. m-LL2 IN RAJI CELLS

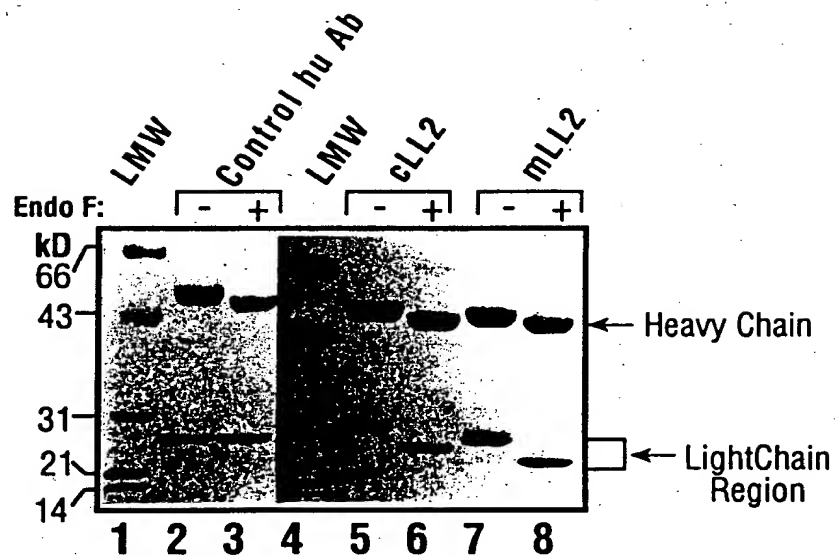


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Inventor(s): Shui-on LEUNG et al.

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FIG. 13



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Inventor(s): Shui-on LEUNG et al.

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FIG. 14

